



IFWO

## RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/759,463

TIME: 14:42:30

Input Set : N:\Crf3\RULE60\10759463.raw.txt

Output Set: N:\CRF4\08302004\J759463.raw

```

1 <110> APPLICANT: Itadani, Hiraku
2     Takimura, Tetsuo
3     Nakamura, Takao
4     Kobayashi, Masahiko
5     Tanaka, Ken-ichi
6     Hidaka, Yusuke
7     Ohta, Masataka
8 <120> TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
9     BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
10 <130> FILE REFERENCE: 06501-083001
11 <140> CURRENT APPLICATION NUMBER: US/10/759,463
12 <141> CURRENT FILING DATE: 2004-01-16
13 <150> PRIOR APPLICATION NUMBER: US/09/891,053
14 <151> PRIOR FILING DATE: 2001-06-25
15 <150> PRIOR APPLICATION NUMBER: PCT/JP99/07280
16 <151> PRIOR FILING DATE: 1999-12-24
17 <150> PRIOR APPLICATION NUMBER: PCT/JP98/05967
18 <151> PRIOR FILING DATE: 1998-12-25
19 <150> PRIOR APPLICATION NUMBER: JP 11/145661
20 <151> PRIOR FILING DATE: 1999-05-25
21 <160> NUMBER OF SEQ ID NOS: 26
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 413
26 <212> TYPE: PRT
27 <213> ORGANISM: Rattus norvegicus
28 <400> SEQUENCE: 1
29     Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
30         1           5           10           15
31     Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
32         20           25           30
33     Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
34         35           40           45
35     Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
36         50           55           60
37     Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
38         65           70           75           80
39     Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
40         85           90           95
41     Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
42         100          105          110
43     Val Asp Tyr Leu Leu Cys Ala Ser Val Phe Asn Ile Val Leu Ile
44         115          120          125

```

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```

45 Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
46      130      135      140
47 Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
48      145      150      155      160
49 Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
50      165      170      175
51 Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
52      180      185      190
53 Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
54      195      200      205
55 Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
56      210      215      220
57 Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
58      225      230      235      240
59 Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Ala Pro Pro
60      245      250      255
61 Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
62      260      265      270
63 His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
64      275      280      285
65 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
66      290      295      300
67 Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
68      305      310      315      320
69 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
70      325      330      335
71 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
72      340      345      350
73 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
74      355      360      365
75 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
76      370      375      380
77 Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
78      385      390      395      400
79 Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
80      405      410

```

82 &lt;210&gt; SEQ ID NO: 2

83 &lt;211&gt; LENGTH: 1239

84 &lt;212&gt; TYPE: DNA

85 &lt;213&gt; ORGANISM: Rattus norvegicus

86 &lt;220&gt; FEATURE:

87 &lt;221&gt; NAME/KEY: CDS

88 &lt;222&gt; LOCATION: (1)...(1239)

89 &lt;400&gt; SEQUENCE: 2

```

90 atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg
91 Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
92      1      5      10      15
93 gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc
94 Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

```

48

96

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Input Set : N:\Crf3\RULE60\10759463.raw.txt

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95		20		25		30		
96	tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca							144
97	Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr							
98		35		40		45		
99	gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tgc agc							192
100	Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser							
101		50		55		60		
102	ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac							240
103	Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp							
104		65		70		75		80
105	ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg							288
106	Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu							
107		85		90		95		
108	acc ggc cgt tgg acc ttc ggc cgg gcc ctc tgc aag ctg tgg ctg gtg							336
109	Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val							
110		100		105		110		
111	gta gac tac cta ctg tgt gcc tcc tgc gtc ttc aac atc gta ctc atc							384
112	Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile							
113		115		120		125		
114	agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc							432
115	Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala							
116		130		135		140		
117	cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg							480
118	Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp							
119		145		150		155		160
120	gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac							528
121	Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr							
122		165		170		175		
123	ctg tct ggt ggc agt tcc atc ccc gag gcc cac tgc tat gct gag ttc							576
124	Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe							
125		180		185		190		
126	ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc							624
127	Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe							
128		195		200		205		
129	acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac							672
130	Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn							
131		210		215		220		
132	atc cag agg cgc acc cgc ctt cgg ctt gat ggg gcc cgt gag gct ggc							720
133	Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly							
134		225		230		235		240
135	cca gaa ccc cca cca gat gcc cag ccc tgc cca cct cca gct ccc ccc							768
136	Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro							
137		245		250		255		
138	agc tgc tgg ggc tgc tgg cca aaa ggg cat gcc gag gcc atg ccg ttg							816
139	Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu							
140		260		265		270		
141	cac agc tct ggc agc tcc tca agg gcc act gag agg cca cgc tca ctc							864
142	His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu							
143		275		280		285		

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Output Set: N:\CRF4\08302004\J759463.raw

```

144   aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc      912
145   Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
146       290                295                300
147   atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tgc cgg      960
148   Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
149       305                310                315                320
150   gac aag aag gtg gcc aag tgc ctg gcc atc atc gtg agc atc ttt ggg      1008
151   Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
152       325                330                335
153   ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc      1056
154   Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
155       340                345                350
156   cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt      1104
157   His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
158       355                360                365
159   ctg tgg gcc aac tgc gcc gtc aac ccc gtc ctc tac cca ctg tgc cac      1152
160   Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
161       370                375                380
162   tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc      1200
163   Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
164       385                390                395                400
165   aag gtc cag ccc cac gcc tcc ctg gag cag tgc tgg aag      1239
166   Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
167       405                410
169 <210> SEQ ID NO: 3
170 <211> LENGTH: 21
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: artificially synthesized primer sequence
W--> 175 <221> NAME/KEY: misc_feature
176 <222> LOCATION: (1)...(21)
177 <223> OTHER INFORMATION: n = A,T,C or G
W--> 178 <400> 3
W--> 179   batngccaac ctbkccttct c      21
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 20
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: artificially synthesized primer sequence
W--> 187 <221> NAME/KEY: misc_feature
188 <222> LOCATION: (1)...(20)
189 <223> OTHER INFORMATION: n = A,T,C or G
W--> 190 <400> 4
W--> 191   ccataaaaagn nggggttgac      20
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 2700
195 <212> TYPE: DNA

```

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Output Set: N:\CRF4\08302004\J759463.raw

```

196 <213> ORGANISM: Rattus norvegicus
197 <220> FEATURE:
198 <221> NAME/KEY: CDS
199 <222> LOCATION: (351)...(1589)
200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: (1)...(2700)
202 <223> OTHER INFORMATION: n = A,T,C or G
V--> 203 <400> 5
204      aattcggcac gagcgggcag atcgcggggc gcactcgggtt gcgcgctgag ctaggggtgc      60
205      accgacgcac cgcggggcgc tggagctcgg ctttgctctc gctgcagcag ccgcgccgcc      120
206      cgccccactc cgctcagatt ccgacaccag cccctctcgg atcgccctcc tggactctag      180
207      cccgggctct tgcctcgacc ccgcggacca tgctccgggc gccccccgga aaaccgggct      240
208      gggcgaagag ccggcaaaga ttaggctcac gagcgggggc cccaccgggc caccagctc      300
209      tccgcccgtg ccctgcccgg tgtccccgag ccgtgtgagc ctgctgggccc atg gag      356
210                                          Met Glu
211                                          1
212      cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg gcc gga      404
213      Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly
214          5                      10                      15
215      gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc tgg acc      452
216      Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr
217          20                      25                      30
218      gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca gta ctg      500
219      Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu
220          35                      40                      45                      50
221      ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc ctc cgc      548
222      Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg
223          55                      60                      65
224      acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac ttc ctc      596
225      Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu
226          70                      75                      80
227      gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg acc ggc      644
228      Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly
229          85                      90                      95
230      cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg gta gac      692
231      Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp
232          100                      105                      110
233      tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc agc tat      740
234      Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr
235          115                      120                      125                      130
236      gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag      788
237      Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln
238          135                      140                      145
239      ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg      836
240      Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu
241          150                      155                      160
242      gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct      884
243      Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser
244          165                      170                      175

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 08/30/2004  
PATENT APPLICATION: US/10/759,463      TIME: 14:42:31

Input Set : N:\Crf3\RULE60\10759463.raw.txt  
Output Set: N:\CRF4\08302004\J759463.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 4  
Seq#:4; N Pos. 10,11  
Seq#:5; N Pos. 2688  
Seq#:11; N Pos. 20  
Seq#:22; N Pos. 18  
Seq#:23; N Pos. 18

VERIFICATION SUMMARY

DATE: 08/30/2004

PATENT APPLICATION: US/10/759,463

TIME: 14:42:31

Input Set : N:\Crf3\RULE60\10759463.raw.txt

Output Set: N:\CRF4\08302004\J759463.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:175 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
 L:178 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
 L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
 L:187 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
 L:190 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4  
 L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
 L:203 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5  
 L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2629  
 L:365 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11  
 L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
 L:679 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
 L:682 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22  
 L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0  
 L:691 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
 L:694 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23  
 L:695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0